

SEQUENCE LISTING

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 Amstutz, Hanspeter



<120> POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING
 STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS,
 THE DNA ENCODING THEM AND THE PROCESS FOR THEIR
 PREPARATION AND USE

<130> 6816/P63221US0

<140> 09/147,443

<141> 1999-01-21

<150> PCT/EP97/03253

<151> 1997-06-20

<150> EP 96810421.6

<151> 1996-06-24

<160> 64

<170> PatentIn Ver. 2.1

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 35 40 45

Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
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 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
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 35 40 45

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 50 55 60

 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp
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Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Thr	Leu	Tyr	
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Ala	Arg	Asp	Lys	Ala	Val	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	
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Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
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Ala	Leu	Ile	Trp	Phe	Asp	Gly	Ser	Ile	Arg	Ser	Tyr	Ala	Glu	Ser	Val
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Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
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 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly
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 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60
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 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
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 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr
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 20 25 30

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 35 40 45

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
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Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr
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 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
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ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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 50 55 60

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 65 70 75 80

ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt 288
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 85 90 95

gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg 336
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
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 35 40 45
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
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 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
 20 25 30

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 Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Phe Ala
 35 40 45

gca tcg aat ttg caa act ggg gtc cca tcc agg ttc agt ggc agt gga 192
 Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

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 65 70 75 80

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 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Arg Pro Phe Thr Phe
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 35 40 45

Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asp Leu Gln Pro Glu Asp
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Ser	Leu	Arg	Leu	Ser	Cys	Ile	Ala	Ser	Gly	Phe	Thr	Leu	Arg	Asn	Tyr	
			20					25					30			
gcc	atg	cac	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggg	ctg	gag	tgg	gtg	144
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Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe	
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ctg	cac	atg	aac	agc	ctg	aga	gcc	gag	gac	acg	gct	aca	tat	tac	tgt	288
Leu	His	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Thr	Tyr	Tyr	Cys	
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gcg	aga	gag	agg	gcg	att	cgg	gga	atc	agt	aga	tac	aat	tac	tac	atg	336
Ala	Arg	Glu	Arg	Ala	Ile	Arg	Gly	Ile	Ser	Arg	Tyr	Asn	Tyr	Tyr	Met	
			100					105					110			
gac	gtc	tgg	ggc	aag	ggg	acc	acg	gtc	acc	gtc	tcc	tca				375
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			20					25					30			
Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
Ala	Gly	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Lys	Asn	Tyr	Ala	Asp	Ser	Val	
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Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe	
	65				70					75				80		

Leu His Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Thr Tyr Tyr Cys
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 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Ser Leu Asn
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 tgg tat cag cag aaa cca ggg aaa gcc cct aaa gtc ctg atc tat gct 144
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Tyr Ala
 35 40 45
 gca tcc agt ttg caa agt ggg gtc cca tcc agg ttc agt ggc aga gga 192
 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly
 50 55 60
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 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
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 35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Arg Gly
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
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Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Ser Ser Trp Thr Phe
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Gly Gln Gly Thr Lys Val Glu Ile Lys
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tcc ctg aga ctt tcc tgt gca gcg tct gga ttc agt ttc aat agc cat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Asn Ser His
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
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 35 40 45

gca ttt ata tgg ttt gat ggc agt aat aaa tac tat gca gac tcc gtg 192
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aag ggc cga ttc acc atc acc aga gac aac tcc aag aac acg ctg tat 240
 Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtc tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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378

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Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35           40           45
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
      50           55           60
Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Tyr
      65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
      85           90           95
Ala Arg Glu Thr Ser Val Arg Leu Gly Tyr Ser Arg Tyr Asn Tyr Tyr
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      115           120           125

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1				5					10					15		
gtc	acc	atc	act	tgc	cgg	gca	agt	cag	agc	att	agg	agc	cat	ttg	aat	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Arg	Ser	His	Leu	Asn	
			20					25					30			
tgg	tat	cag	cag	aaa	cca	ggg	aaa	gcc	cct	aag	ctc	ctg	atc	tat	gct	144
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				

gca tcc agt ttg caa ggt ggg gtc cca tca agg ttc agt ggc agt gga 192
 Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

ttt gca act tat tac tgt caa cag agt tac agg gcc cct cag tgg acg 288
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr
 85 90 95

ttc ggc caa ggg acc aag gtg gaa atc aaa 318
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 20
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 20
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn
 20 25 30
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45
 Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ala Pro Gln Trp Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 21
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(375)

<400> 21

cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ctc agg agt tat 96
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg gtc tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr
 65 70 75 80

ctg caa atg aac agc ctg aga gcc gat gac acg gct gta tat tat tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gag aag gcg ctt cgg gga atc agc aga tac aac tat tac ctg 336
 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110

gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 22

<211> 125

<212> PRT

<213> Homo sapiens

<400> 22

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
		115					120					125

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<210> 23
<211> 333
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1) .. (333)
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<400> 23																
gtg	gtg	act	cag	cca	ccc	tca	gcg	tct	ggg	acc	ccc	gga	cag	agg	gtc	48
Val	Val	Thr	Gln	Pro	Pro	Ser	Ala	Ser	Gly	Thr	Pro	Gly	Gln	Arg	Val	
1				5				10						15		
acc	atc	tct	tgt	tct	gga	agc	aac	tcc	atc	ctt	gga	agt	aag	tat	gta	96
Thr	Ile	Ser	Cys	Ser	Gly	Ser	Asn	Ser	Ile	Leu	Gly	Ser	Lys	Tyr	Val	
		20						25						30		
tac	tgg	tac	cag	aaa	ctc	cca	gga	acg	gcc	ccc	aaa	ctc	ctc	atc	tat	144
Tyr	Trp	Tyr	Gln	Lys	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	
		35						40						45		
aag	aat	gat	cag	cgg	ccc	tca	ggg	gtc	tct	gac	cga	ttc	tct	ggc	tcc	192
Lys	Asn	Asp	Gln	Arg	Pro	Ser	Gly	Val	Ser	Asp	Arg	Phe	Ser	Gly	Ser	
50						55						60				
aag	tct	ggc	acc	tcg	gcc	tcc	ctg	gcc	atc	agt	ggg	ctc	cgg	tcc	gag	240
Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Ser	Gly	Leu	Arg	Ser	Glu	
65				70						75				80		
gat	gag	gct	gac	tat	tac	tgt	gca	cca	tgg	gat	gcc	aac	ctg	ggt	ggc	288
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Pro	Trp	Asp	Ala	Asn	Leu	Gly	Gly	
				85						90				95		
ccg	gtg	ttc	ggc	gga	ggg	acc	aag	ctg	acc	gtc	cta	agt	cag	ccc		333
Pro	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Ser	Gln	Pro		
		100						105						110		

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<210> 24
<211> 111
<212> PRT
<213> Homo sapiens
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<400> 24
Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
  1                               10                               15
Thr Ile Ser Cys Ser Gly Ser Asn Ser Ile Leu Gly Ser Lys Tyr Val
                20                25                30

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Tyr Trp Tyr Gln Lys Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Lys Asn Asp Gln Arg Pro Ser Gly Val Ser Asp Arg Phe Ser Gly Ser
 50 55 60
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu
 65 70 75 80
 Asp Glu Ala Asp Tyr Tyr Cys Ala Pro Trp Asp Ala Asn Leu Gly Gly
 85 90 95
 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
 100 105 110

<210> 25
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(375)

<400> 25
 cag gtg aaa ctg ctc gag tcg ggg gga ggc gtg gtc cag ccg ggg ggg 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct 96
 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60
 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt 288
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg 336
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110
 gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 26
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 26
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 27
 <211> 312
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(312)

<400> 27
 gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga 48
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15
 gtc acc atc act tgc cgg aca agt cag acc att agc aga aat tta aat 96
 Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn
 20 25 30
 tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45
 aca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
 Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

tct ggg aca gat ttc act ctc acc atc aat agt cta caa cct gaa gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp
 65 70 75 80

ttt gca act tac tac tgt caa cag agt tac act acc cct tcg ttc ggc 288
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly
 85 90 95

caa ggg acc aag gtg gaa atc aaa 312
 Gln Gly Thr Lys Val Glu Ile Lys
 100

<210> 28
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 28
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

Val Thr Ile Thr Cys Arg Thr Ser Gln Thr Ile Ser Arg Asn Leu Asn
 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45

Thr Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ser Phe Gly
 85 90 95

Gln Gly Thr Lys Val Glu Ile Lys
 100

<210> 29
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(375)

<400> 29
 cag gtg aaa ctg ctc gag tct ggg gga ggc ttg gtc cag ccg ggg ggg 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ttc agg agt tat 96
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg ctc tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
 65 70 75 80

ctg caa atg aat agc ctg aga gcc gag gac acg gct gta tat tat tgt 288
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg 336
 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110

gac gtc tgg ggc aag ggg gcc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser
 115 120 125

<210> 30
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 30
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110

Asp Val Trp Gly Lys Gly Ala Thr Val Thr Val Ser Ser
 115 120 125

<210> 31
 <211> 318
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(318)

<400> 31
 gtg atg acc cag tct cca tcc tcc ctg tct gca tct ata ggc gac aga 48
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
 1 5 10 15
 gtc acc atc act tgc cgg gca agt cag agc gtt acc agg tct tta aat 96
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn
 20 25 30
 tgg tat cag cag aaa cca ggg aaa gcc cct agg ctc cta atc ttt gct 144
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala
 35 40 45
 gcg tcc act ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60
 tct ggg aca gat ttc acc ctc acc atc agc agt ctg caa cct gag gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80
 ttt gga act tac tac tgt caa cag aat tac agg acc cct cag tgg acg 288
 Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr
 85 90 95
 ttc ggc caa ggg acc aag gta gaa atc aaa 318
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 32
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 32
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly Asp Arg
 1 5 10 15
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Thr Arg Ser Leu Asn
 20 25 30
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Phe Ala
 35 40 45
 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Gly Thr Tyr Tyr Cys Gln Gln Asn Tyr Arg Thr Pro Gln Trp Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 33
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (378)

<400> 33
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ctc agg agt tat 96
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr
20 25 30
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
50 55 60
aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac atg gtc tat 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr
65 70 75 80
ctg caa atg aac agc ctg aga gcc gat gac acg gct gta tat tat tat 288
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr
85 90 95
tgt gcg aga gag aag gcg ctt cgg gga atc agc aga tac aac tat tac 336
Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr
100 105 110
ctg gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 378
Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 34
<211> 126
<212> PRT

<213> Homo sapiens

<400> 34

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Leu Arg Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Tyr
 85 90 95

Cys Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr
 100 105 110

Leu Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 35

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (333)

<400> 35

gtg gtg act cag gag ccc tca ctg act gtg tcc cca gga ggg aca gtc 48
 Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
 1 5 10 15

act ctc acc tgt gct tcc agc act ggg gca gtc acc agg ggt tac tat 96
 Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr
 20 25 30

cca aac tgg ttc cag cag aag cct gga caa gca ccc agg gca ctg att 144
 Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile
 35 40 45

tat agt aca aac aaa aaa cac tcc tgg acc cct gcc cgg ttc tca ggc 192
 Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly
 50 55 60

tcc ctc ctt ggg ggc aaa gct gcc ctg aca ctg tca ggt gtg cag cct 240
 Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
 65 70 75 80

gaa gac gag gct gaa tat tac tgc ctg ctc tac tat ggt ggt gct caa 288
 Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln
 85 90 95

ctc gta ttc ggc gga ggg acc aag ctg acc gtc cta cgt cag ccc 333
 Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro
 100 105 110

<210> 36
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 36
 Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val
 1 5 10 15

Thr Leu Thr Cys Ala Ser Ser Thr Gly Ala Val Thr Arg Gly Tyr Tyr
 20 25 30

Pro Asn Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Ala Leu Ile
 35 40 45

Tyr Ser Thr Asn Lys Lys His Ser Trp Thr Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro
 65 70 75 80

Glu Asp Glu Ala Glu Tyr Tyr Cys Leu Leu Tyr Tyr Gly Gly Ala Gln
 85 90 95

Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro
 100 105 110

<210> 37
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(375)

<400> 37
 cag gtg aaa ctg ctc gag tcg ggg gga ggc gtg gtc cag ccg ggg ggg 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct 96
 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
 20 25 30

ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt 288
 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg 336
 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 38

<211> 125

<212> PRT

<213> Homo sapiens

<400> 38

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125


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<220>  
<221> CDS  
<222> (1) .. (315)
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gtg	ttg	acc	cag	tct	cca	tcc	tcc	ctg	tct	gca	tct	ata	cga	gac	aga	48
Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Ile	Arg	Asp	Arg	
1				5				10					15			
gtc	acc	atc	act	tgc	cgg	gca	agt	cag	aac	att	ggc	agt	tat	tta	aat	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Gly	Ser	Tyr	Leu	Asn	
			20					25					30			
tgg	tat	cag	cac	aaa	cca	ggg	aca	gcc	cct	aaa	ctc	ctg	atc	tat	gct	144
Trp	Tyr	Gln	His	Lys	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	
		35					40					45				
gta	tcc	gct	ttg	caa	agt	ggg	gtc	cca	tcg	agg	ttc	agt	ggc	agt	aga	192
Val	Ser	Ala	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Arg	
	50					55				60						
tct	ggg	aca	gat	ttc	act	ctc	acc	atc	agc	agt	ctg	caa	cct	gaa	gat	240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
65					70				75					80		
ttt	gca	act	tac	tac	tgt	caa	cag	agt	tac	agt	ccc	ccg	tac	act	ttc	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Ser	Pro	Pro	Tyr	Thr	Phe	
				85				90					95			
ggc	cag	ggg	acc	aac	ctg	cag	atc	aaa								315
Gly	Gln	Gly	Thr	Asn	Leu	Gln	Ile	Lys								
			100					105								

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<210> 40
<211> 105
<212> PRT
<213> Homo sapiens
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Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Ile	Arg	Asp	Arg
1				5					10					15	
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Gly	Ser	Tyr	Leu	Asn
			20					25					30		
Trp	Tyr	Gln	His	Lys	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala
		35					40					45			
Val	Ser	Ala	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Arg
	50					55					60				

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Pro Pro Tyr Thr Phe
85 90 95

Gly Gln Gly Thr Asn Leu Gln Ile Lys
100 105

<210> 41
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (375)

<400> 41
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15
tcc ctg aga gtc gcc tgt gta gcg tct gga ttc acc ttc agg aat ttt 96
Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
20 25 30
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt 192
Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
50 55 60
aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat 240
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt 288
Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
gcg aga gag aag gcg gtt cgg gga att agt aga tac aac tac tac atg 336
Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
100 105 110
gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375
Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 42
<211> 125
<212> PRT
<213> Homo sapiens

<400> 42

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 43

<211> 315

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (315)

<400> 43

gtg atg acc cag tct cca tcc tcc ctg tct gca tct gtg gga gac aga 48
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

gtc acc atc act tgc cgg gca agt cag agc att atc aac aat tta aat 96
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn
 20 25 30

tgg tat cag cag aaa cca ggc aaa gcc cct gaa ctc ctg atc tat gct 144
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala
 35 40 45

gca tcc agt ttg caa agt ggg gtc cct tca agg ttc cgt ggc agt gga 192
 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly
 50 55 60

tct ggg aga gat ttc act ctc acc gtc acc agt ctg caa cct gaa gat 240
 Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp
 65 70 75 80

ttt gca act tac tac tgt caa cag agt tac agt acc ctg tgg acg ttc 288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe
85 90 95

ggc caa ggg acc aag gtg gaa atc aaa 315
Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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<210> 44
<211> 105
<212> PRT
<213> Homo sapiens
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<400> 44
Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
      1              5              10              15
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Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Asn Asn Leu Asn
20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr Ala
35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly
50 55 60

Ser Gly Arg Asp Phe Thr Leu Thr Val Thr Ser Leu Gln Pro Glu Asp
65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Trp Thr Phe
85 90 95

Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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<210> 45
<211> 375
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)..(375)
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<400> 45
cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

tcc	ctg	aga	ctc	tcc	tgt	gta	gcg	tct	gga	ttc	acc	ttc	agg	agt	tat	96
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Ser	Tyr	
			20					25					30			

ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac acg ctc tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aag agc ctg aga gcc gag gac acg gct gta tat tat tgt 288
 Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg 336
 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110

gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 46

<211> 125

<212> PRT

<213> Homo sapiens

<400> 46

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 47

<211> 315

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (315)

<400> 47

gtg atg acc cag tct cca ttc tcc ctg tct gca tct gta gga gac aga	48
Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
gtc acc atc act tgc cgg gca agt cag aac att agg agt ttt tta agt	96
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser	
20 25 30	
tgg tat cag cag aaa cca ggg aca gcc cct aag ctc ctg atc tat gct	144
Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala	
35 40 45	
gca tcc agg ttg caa agt ggg gtc cca tca agg ttc agt ggc agt ggg	192
Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
tct ggg aca gat ttc act ctc acc atc agc act ctg caa cct gaa gat	240
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp	
65 70 75 80	
ttt gcg act tac tac tgt caa cag agt tac agt gcc cct tgg acg ttc	288
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe	
85 90 95	
ggc caa ggg acc aag ctg gaa atc aaa	315
Gly Gln Gly Thr Lys Leu Glu Ile Lys	
100 105	

<210> 48

<211> 105

<212> PRT

<213> Homo sapiens

<400> 48

Val Met Thr Gln Ser Pro Phe Ser Leu Ser Ala Ser Val Gly Asp Arg	
1 5 10 15	
Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Arg Ser Phe Leu Ser	
20 25 30	
Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ala	
35 40 45	
Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly	
50 55 60	
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Leu Gln Pro Glu Asp	
65 70 75 80	
Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Trp Thr Phe	
85 90 95	

Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 49
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (375)

<400> 49
 cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc tcc agg agt tat 96
 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggc ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gct ttt ata tgg ttt gat gga agt aat aaa gga tat gta gac tcc gtg 192
 Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60
 aag ggc cga ttc acc atc tcc cga gac aat tcc aag aac acg ctc tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ctg caa atg aag agc ctg aga gcc gag gac acg gct gta tat tat tgt 288
 Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gag aag gcg ctt cgg gga atc agt aga tac aac tat tac ctg 336
 Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110
 gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 50
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 50
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Ser Arg Ser Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Gly Ser Asn Lys Gly Tyr Val Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Lys Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Lys Ala Leu Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Leu
 100 105 110

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 51
 <211> 315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(315)

<400> 51
 gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga 48
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

gtc acc atc act tgc cgg gca agt cag agc att agc agc tat tta aat 96
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
 20 25 30

tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45

gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

ttt gca act tac tac tgt caa cag agt tac agt acc cga ttc act ttc 288
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe
 85 90 95

ggc cct ggg acc aaa gtg gat atc aaa
 Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

315

<210> 52
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 52
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
 20 25 30
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45
 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Arg Phe Thr Phe
 85 90 95
 Gly Pro Gly Thr Lys Val Asp Ile Lys
 100 105

<210> 53
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) .. (384)

<400> 53
 cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag cct ggg agg 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 tcc ctg aga ctt tcc tgt gca gcg tct gga ttt acc ttc agt agc tat 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gca gat ata tgg ttt gat gga ggt aat aaa cat tat gca gac ttc gtg 192
 Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val
 50 55 60

aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg gtg tat 240
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80

cta caa atg aac agc ctg aga gtc gag gac acg gct gtg tat tac tgt 288
 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg agg gat tac tat agc gtt act aag aaa ctc aga ctc cac tac tac 336
 Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr
 100 105 110

tac tac atg gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca 384
 Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 54
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 54
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Asp Ile Trp Phe Asp Gly Gly Asn Lys His Tyr Ala Asp Phe Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Tyr Tyr Ser Val Thr Lys Lys Leu Arg Leu His Tyr Tyr
 100 105 110
 Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 55
 <211> 315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(315)

<400> 55

gtg atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga 48
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

gtc acc atc act tgc cgg gca agt cag ggc att aga aat gat tta acc 96
 Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr
 20 25 30

tgg tat cag caa aaa cca ggg aaa gcc cct aag ctc ctg atc tat gct 144
 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45

gca tcc aat tta caa agt ggg gtc cca tca agg ttc agc ggc agt gga 192
 Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

tct ggc aca gat ttc act ctc acc atc agc agc ctg cag cct gaa gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

ttt gca act tat tac tgt cta caa gat aac aat ttc ccg tac act ttt 288
 Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe
 85 90 95

ggc cag ggg acc aag ctg gag atc aaa 315
 Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 56

<211> 105

<212> PRT

<213> Homo sapiens

<400> 56

Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Thr
 20 25 30

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 35 40 45

Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Asn Asn Phe Pro Tyr Thr Phe
 85 90 95

Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 57
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(375)

<400> 57
 cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga gtc gcc tgt gta gcg tct gga ttc acc ttc agg aat ttt 96
 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt 192
 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60
 aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat 240
 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt 288
 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 gcg aga gag aag gcg gtt cgg gga att agt aga tac aac tac tac atg 336
 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110
 gac gtc tgg ggc aag ggg acc acg gtc acc gtc tcc tca 375
 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 58
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 58
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30

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<210> 59
<211> 315
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)..(315)
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<400> 59																
gtg	atg	acc	cag	tct	cca	tcc	tcc	ctg	tct	gca	tct	gta	gga	gac	aga	48
Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	
1				5				10						15		
<400> 96																
gtc	acc	atc	act	tgc	cgg	gca	agt	cag	agc	att	atc	aga	tat	tta	aat	96
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ile	Arg	Tyr	Leu	Asn	
			20					25					30			
<400> 144																
tgg	tat	cag	cac	aaa	cca	ggg	aaa	gcc	cct	aag	ctc	ctg	atc	cat	act	144
Trp	Tyr	Gln	His	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	His	Thr	
		35					40					45				
<400> 192																
gca	tcc	agt	ttg	caa	agt	ggg	gtc	ccg	tca	agg	ttc	agt	ggc	agt	gta	192
Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Val	
	50					55					60					
<400> 240																
tct	ggg	aca	gat	ttc	act	ctc	acc	atc	agc	agt	ctg	caa	cct	gaa	gat	240
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	
65				70						75				80		
<400> 288																
ttt	gca	act	tac	tac	tgt	caa	cag	agt	tac	act	acc	ccg	tac	act	ttt	288
Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Thr	Thr	Pro	Tyr	Thr	Phe	
				85					90					95		
<400> 315																
ggc	cag	ggg	acc	aag	ctg	cag	atc	aaa								315
Gly	Gln	Gly	Thr	Lys	Leu	Gln	Ile	Lys								
			100					105								

<210> 60
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 60
 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
 20 25 30
 Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Thr
 35 40 45
 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
 50 55 60
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe
 85 90 95
 Gly Gln Gly Thr Lys Leu Gln Ile Lys
 100 105

<210> 61
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(375)

<400> 61
 cag gtg aaa ctg ctg gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aga gtc gcc tgt gta gcg tct gga ttc acc ttc agg aat ttt 96
 Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30
 ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 gct ttt att tgg ttt gat gca agt aat aaa gga tat gga gac tcc gtt 192
 Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60

aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctc tat 240
 Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

ctg caa atg aac ggc ctg aga gcc gaa gac acg gct gta tat tat tgt 288
 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gcg aga gag aag gcg gtt cgg gga att agt aga tac aac tac tac atg 336
 Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
 100 105 110

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 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
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<211> 125

<212> PRT

<213> Homo sapiens

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Ser Leu Arg Val Ala Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Phe
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Phe Ile Trp Phe Asp Ala Ser Asn Lys Gly Tyr Gly Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
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Ala Arg Glu Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
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Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
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gtc acc atc act tgc cgg gca agt cag agc att atc aga tat tta aat 96
 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
 20 25 30

tgg tat cag cac aaa cca ggg aaa gcc cct aag ctc ctg atc cat gct 144
 Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala
 35 40 45

gca tcc agt ttg caa agt ggg gtc ccg tca agg ttc agt ggc agt gta 192
 Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
 50 55 60

tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct gaa gat 240
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

ttt gca act tac tac tgt caa cag agt tac act acc ccg tac act ttt 288
 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe
 85 90 95

ggc cag ggg acc aag ctg cag atc aaa 315
 Gly Gln Gly Thr Lys Leu Gln Ile Lys
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<210> 64

<211> 105

<212> PRT

<213> Homo sapiens

<400> 64

Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ile Arg Tyr Leu Asn
 20 25 30

Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile His Ala
 35 40 45

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Val
 50 55 60

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 65 70 75 80

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Tyr Thr Phe
 85 90 95

Gly Gln Gly Thr Lys Leu Gln Ile Lys
 100 105